AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

1-21. (cancelled)

22. (currently amended) A method for gene mapping to locate a gene associated with a certain phenotype from a dataset of chromosome and phenotype data ~~from a database, comprising analyzing linkage disequilibrium between~~ by analyzing an association between phenotype and genetic ~~marks~~ markers m_i, comprising:

i) searching from ~~the data~~ said dataset for all marker patterns P that satisfy a pattern evaluation function $e(P)$, wherein

a: the marker patterns are expressions within ~~the database~~ said dataset comprising genetic markers and their alleles and zero or more of the following: individual covariates, environmental variables and auxiliary phenotypes; and

b: the pattern evaluation function $e(P)$ is a measure of the association between the marker pattern P and a phenotype being studied,

ii) scoring each marker m_i of the data with a marker score $s(m_i)$, which is a function of the set S_i defined as the set of marker patterns overlapping the marker m_i and satisfying the pattern evaluation function e as defined in step i), and

iii) ~~mapping the location of a gene by evaluating the scores $s(m_i)$ of all the markers m_i in the data which is determined by maximizing the score if the scoring function is designed to give higher scores closer to the gene, and on minimizing the score if the scoring function is designed to give lower scores closer to the gene~~ locating said gene to the marker m_i having the best score $s(m_i)$, wherein the best score is the highest obtained score if said scoring function is designed to give higher scores closer to the gene, or the lowest obtained score if said scoring function is designed to give lower scores closer to the gene, or locating said gene to a chromosomal region containing a set of best scoring markers.

23. (previously presented) The method of claim 22, wherein the chromosome data consists of either haplotypes or genotypes.

24. (previously presented) The method of claim 23, wherein said haplotypes and genotypes contain flexible regions.

25-29. (cancelled)

30. (currently amended) The method of claim 22, wherein

a) the phenotype being studied is qualitative, and

b) the pattern evaluation function $e(P)$ has the form $e(P) = true\ if\ and\ only\ if\ e'(P) > x$, where $e'(P)$ is the ~~(signed)~~ signed association measure χ^2 and x is a user specified minimum value wherein said signed value of the χ^2 is negative if the

relative frequency of the halotype pattern among the control chromosomes is higher than that of the trait-associatead chromosomes, and otherwise positive, and

c) the score $s(m_i)$ of marker m_i is the size of S_i, also called marker-wise pattern frequency of m_i and denoted by $f(m_i)$.

31. (previously presented) The method of claim 22, wherein

a) the pattern evaluation function $e(P)$ has the form $e(P)$ = *true if and only if* $e'(P) > x$, where $e'(P)$ is the absolute frequency of pattern P in the data and x is a user-specified value,

b) in order to derive the score $s(m_i)$, the p value (statistical significance) of each marker pattern P in determining the phenotype being studied is evaluated, and

c) the score $s(m_i)$ is the distance between the observed p value distribution of patterns in S_i and the uniform distribution, defined as average of $(p_i - q_i) \log (p_i / q_i)$ over all $i = 1..n$, where n is the number of haplotype patterns in S_i, p_i is the ith smallest p value in S_i, and q_i is the expectation of the ith smallest p value, if the p values were randomly drawn from the uniform distribution.

32. (previously presented) The method of claim 31, where the p value is computed using a linear model of form $Y = \beta_1 X_1 + \ldots + \beta_k X_k + \alpha Z + \beta_0$, where the dependent variable Y is the phenotype

being studied, X_1 through X_k are covariates, and Z is a dummy variable for the occurrence of the haplotype pattern, and the coefficients α and β_* are adjusted for best fit, and then the significance of Z as a covariate is assessed using a t test with the null hypothesis "$\alpha = 0$".

33. (previously presented) The method of claim 22, further refining each score $s(m_i)$ by replacing it by the marker-wise p value of the score $s(m_i)$, where the statistical significance of $s(m_i)$ is measured against the null hypotheses that there is no gene effect.

34. (previously presented) The method of claim 22, wherein an area returned from a prediction of a gene location is contiguous or fragmented or a point.

35-38. (canceled)

39. (previously presented) A computer-readable data storage medium having computer-executable program code stored thereon operative to perform the method of claim 22 when executed on a computer.

40. (previously presented) A computer system having executable program code that performs the method of claim 22.